

JOINT ANALYSIS OF DIFFERENT VIEWS OF MAMMOGRAPHIC IMAGES

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I Introduction

Breast cancer is one of the most frequent cancers and the leading cause of mortality for women, affecting almost one eighth of them and giving one third of cancers. Evidences show that X-ray mammography is the only reliable screening method giving nearly 95% chance of survival within 5 years due to early detection. [1] Due to the huge number of images captured per year and the high number of false positive diagnoses done by doctors (80-93%), development of mammographic decision support systems is under heavy research.

According to the importance of the topic numerous researches are going on about the topic including development of computer aided diagnosis (CAD) systems – a special part of which I have started investigating during writing my master degree.

This article is going to follow the order of this research: first I started and investigating the importance of joint analysis, then cooperating with Márta Altrichter we created a reference system to pair areas on different views of mammographic images, later on we realized that microcalcifications and masses need separate methods for joint analysis due to their different characteristics, and in my latest publication I have been focusing on improvement of results by giving stressed attention to spiculated massed that could be paired with less efficiency. During my work I also tried to keep algorithms usable by shortening running times.

II Importance of Joint Analysis

During X-ray screening two different views are captured of each breast: a CC (cranio-caudal) from above and a leaning lateral view, the MLO. The two most important symptoms are microcalcifications (small spots that have high intensity compared to their environment) and masses (big, high intensity blobs) – note that since X-ray images are inverted, high intensity spots are shades in fact. Our results and other publications on this topic show that obtaining high hit rate while keeping the number of false positive detections low is extremely difficult. [1]

Microcalcification and mass detector algorithms developed in our department have quite a good hit rate (near 95%) but the false positive hits per image are 3 per image in the case of microcalcifications and 6 in the case of masses. [2,3] This false positive rate can be reduced if – in addition to the individual analysis – joint analysis of the images is done similarly to the way done by radiologist experts. Finding a pair to a mass- or microcalcification-candidate on the other view can increase the probability that the hit is a true positive one, therefore it should be kept. On the other hand – if no pair is found, the candidate can be regarded as a false positive one.

(We assumed that this neglection should be done considering breast density. Up to this time the latter detailed algorithm works with similar performance for all groups of densities.)

III Basics of Joint Analysis

Since in X-ray mammography perfect 3-D reconstruction is impossible due to breast deformation, we implemented a simple “2.5-D” positioning system between CC and MLO images for this joint analysis. This means that we can assign a stripe on the MLO image to every mass-candidate on the CC image and vice versa. The stripe is based on the position of the nipple and the angle of the pectoral muscle. According to this reference system we could make a hypothesis: “the *distances* of a mass (measured from the tangent that is parallel to the pectoral muscle and placed in the nipple) in the CC and MLO pictures are nearly equal”.

We used EdgeFlow [5] for finding the pectoral muscle since this edge detecting algorithm is also used in further steps, but according to other authors lots of other techniques can also be used, for example Hugh transformation.

The correctness of the reference system and our hypothesis were tested by a statistical analysis. Results showed that the assumption was correct though there is some variance caused by the failures of the algorithm, wrong radiologist assessment or the flaw of the hypothesis (because of breast deformation) for a few cases. To compensate these effects the width of the stripe can be increased by a constant or by a number relative to the width of the stripe to counteract the deviation of the algorithm. According to our experiments a margin of 30 pixels have proven to be the best choice with an offset of 10 pixels. (We used images with 400 micron resolution, since on this resolution all masses are visible but running times are still tolerable.)

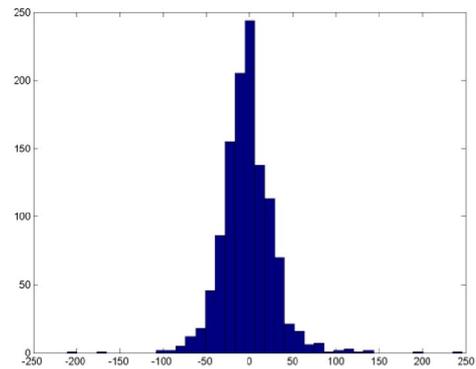


Figure 1. Histogram of error
(horizontal axis: error of hypothesis in pixels
vertical axis: number of occurrences in test set)

IV Joint Analysis for Masses

Since masses have characteristic texture, the reference system can be improved by textural analysis. (Some parts of the breast within the stripe can obviously not be the pair – based on texture features – of the examined mass candidate.) This is done through the following steps (see Fig. 2 also):

1. First the image is segmented by EdgeFlow [5], and then texture features (based on intensity, co-occurrence and gray-level-differences) are calculated for each segment, k-means clustering is applied to these features resulting a better segmentation.
2. Once we have a good quality segmentation, we recalculate features for the new segments.
3. After these preliminary steps we establish the reference system.
4. Then for each mass-candidate (b) we do pairing by computing the corresponding stripe (e) and – based on texture features – we choose the most similar segments within the stripe (f,g&h). (Note that based on some rule-based laws this pairing may result no pair at all. This decision mainly contains size, intensity, texture similarity based rules.)
5. For the given mass candidate we check if there are pairs colliding with candidates on the other image. This pairing is done in both ways. Only those mass-candidates are kept which have a pair found. (Since (h) confirms candidate on (d), we keep it.)

With this algorithm we could achieve that 92% of true positive hits are kept while 23% of false positives are neglected.

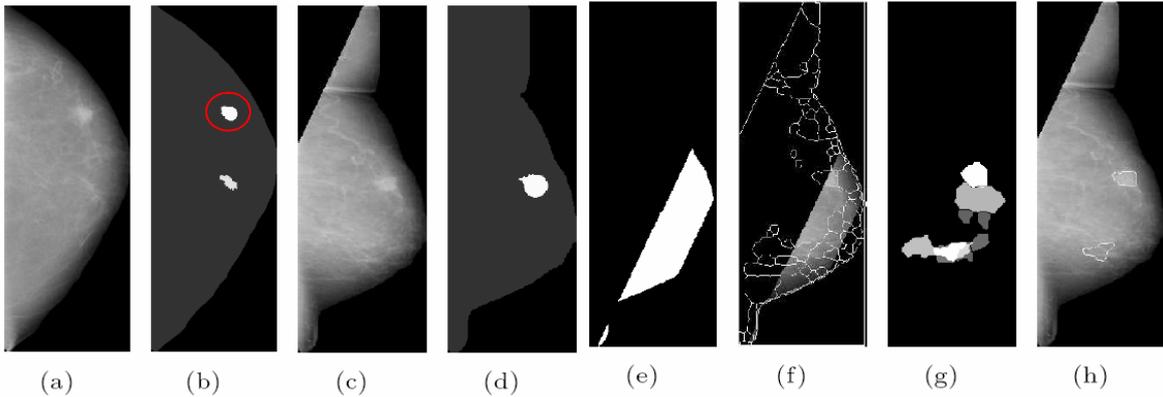


Figure 2. (a&c) CC & MLO image, (b&d) mass candidates on CC & MLO (marked candidate examined), (e) corresponding stripe to marked candidate, (f) segmentation (highlighted within stripe), (g) segments on MLO (intensity proportional to textural similarity), (h) possible pairs

V Focusing on Spiculated Masses

We have found that some spiculated masses cannot be well distinguished from normal tissue, since most of our previously used texture features are based on some derivatives of intensity and these masses have no high intensity core but only a stellar form causing our algorithm to draw false conclusions. Therefore we investigated the related references for clever techniques or distinctive texture features. After some unsuccessful trials we have found that ALOE invented by Kegelmayer et al. [6] can be used for our aims.

ALOE (Analysis of Local Oriented Edges) is based on the following facts. Spiculated masses have a stellar form, while normal breast tissue usually has mostly parallel linear structures (at the scale of usual segments) aiming at one direction. Therefore a histogram of pixelwise edge orientations having numerous local maxima is characteristic for spiculated segments, and a histogram having some local maximums should belong to normal segments. This difference can be well characterized by the variance of this histogram.

ALOE can be parametrized along edge detection: one can use any kind of edge detecting algorithm to gain pixelwise local orientation. References mention two groups of filters: classical edge detecting algorithms (filters of Prewitt, Roberts, Laplace, etc.) and Gaussian derivatives. We have also tried these methods and naturally investigated the usability of some results of EdgeFlow.

Both in our early experiments on cut image segments, and latter detailed tests when we built this feature in the pairing algorithm proved that the best choice is the EdgeFlow based ALOE.

This is due to the fact that classical edge detecting algorithms result mainly in noise for “flat” images segments (where linear structures are further than the scope of the differential filter). Therefore the histogram of local orientations is also flat, just like it should be for spiculated masses. All in all – the main problem with these filters is that the number of pixels having meaningful information about local orientation is low.

However – phase image produced by EdgeFlow has meaningful information even far from edges and also more reliable due to its noise reduction techniques. (Phase detection is based on an error-prediction scheme, and its clever edge-energy vector propagation also has noise reducing effects.)

Comparing results of this modified pairing (including ALOE as texture feature) to our previous results we have found that false positive neglecting rose from 23% to 31% while still keeping 92% of true positive mass candidates. For the sake of comparison: the gain is merely 1-2% with classical edge detecting algorithms; and by only an extra 20% running time in pairing 5% with Gaussian derivatives. This extra running time came from the fact that using pure Gaussians results in 5% gain only if we use 32 orientations instead of 8 used for EdgeFlow. This should be a 4 times factor in

running times but since EdgeFlow has further steps, it causes only this 20% gain. However – note that the results of EdgeFlow are given – due to earlier steps!

In my experiments I have also tried to use a function that is based on both pixelwise energy and orientation – that is a kind of “weighted histogram” – but this led to no increase in performance.

Note that the ALOE value is also low for normal high intensity masses since they have a clear contour, resulting in a wide range of orientations in the filtered image. So we could say that ALOE is conservative regarding our previous feature space. It still keeps non-spiculated masses close in feature space while separates spiculated ones from normal tissue – that had previously proven to be too close.

VI Performance in Time

As it can be seen from the results above – it proved to be true that such an analysis can improve performance but since running times are high, the approach cannot be used yet. Therefore we also focused our efforts on accelerating algorithms while keeping performance at least at the same level. This is partly a technical, partly substantive question since for better running times it is not enough to use clever coding techniques but some algorithms had to be substantially modified. (However – faster running has one benefit. There are always some free parameters that affect performance, and therefore should be carefully tuned. With less running time a more exhaustive testing can be done during the same amount of time.)

Up to the time of present article running times declined to half to the original, while – according to the tests – performance is still as good as it was in the beginning. This means about 10 minutes of running time per pairs of images.

VII Summary and Future work

During my research I have managed to prove that there is a way of applying joint analysis on different views of mammographic images even though perfect 3D reconstruction is impossible. With the help of this joint analysis a remarkable percentage of false positive mass-candidates can be eliminated by much smaller loss of true positive ones. I also succeeded in improving a special texture feature for spiculated masses.

Lately I have been working on applying intelligent learning methods for pairing instead of rule based systems and also plan numerous tests to draw detailed ROC curves on performance.

References

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